In the Claims

Please amend the claims as follows:

1-23. (Cancelled)

24. (Currently amended) ~~The method of claim 23,~~ A method for identifying elite event MS-B2 in a transgenic *Brassica* plant, or cell or tissue thereof, or transgenic *Brassica* plant material, said method comprising amplifying a DNA fragment of between 100 and 300 nucleotides ~~160 and 200 by~~ from a nucleic acid present in said transgenic *Brassica* plant, or cell or tissue thereof, or transgenic *Brassica* plant material, using a polymerase chain reaction (PCR) with a first specific primer or probe ~~at least two primers, one of~~ which comprises at least 16 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in ~~hybridizes to~~ bases 1-234 of SEQ ID NO:8, or the complement thereof, or from the 3' flanking region of MS-B2, comprised in ~~to~~ bases 194-416 of SEQ ID NO:10, or the complement thereof; ~~of MS-B2~~, and a second specific primer or probe ~~the other of~~ which comprises at least 16 consecutive nucleotides from the foreign DNA in MS-B2, or the complement thereof, said foreign DNA corresponding to ~~hybridizes to~~ a sequence within SEQ ID NO:1; and thus identifying a *Brassica* plant, or cell or tissue thereof, or transgenic plant material comprising elite event MS-B2, if said genomic DNA amplifies the DNA fragment using PCR with the primers ~~and detecting said amplified DNA fragment on an agarose gel~~.

25. (Currently amended) The method of claim 24, wherein ~~one of~~ said second specific primer or probe ~~primers hybridizes to a sequence within SEQ ID NO:1 and~~ comprises the sequence of SEQ ID NO: 12.

26. (Currently amended) The method of claim 24, wherein ~~one of~~ said first specific primer or probe comprises at least 16 consecutive nucleotides from the 3' flanking region of MS-B2, comprised in ~~primers hybridizes to~~ bases 194-416 of SEQ ID NO:10, or the complement thereof ~~and comprises the sequence of SEQ ID NO:11~~.

27-29. (Cancelled)

30. (Currently amended) ~~The kit of Claim 29, which further comprises at least~~ A kit for identifying elite event MS-B2 in a transgenic *Brassica* plant, or cell or tissue thereof, or transgenic *Brasscia* plant material, said kit comprising at least a first PCR primer or probe and a second PCR primer or probe, wherein the first PCR primer or probe comprises at least 16 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in bases 1-234 of SEQ

ID NO:8, or the complement thereof, or from the 3' flanking region of MS-B2, comprised in bases 194-416 of SEQ ID NO:10, or the complement thereof; and a second specific primer or probe which comprises at least 16 consecutive nucleotides from foreign DNA of MS-B2, or the complement thereof, said foreign DNA corresponding ~~hybridizes~~ to a sequence within SEQ ID NO:1 ~~of MS-B2~~.

31. (Currently amended) The kit of claim 30, wherein said second ~~at least one~~ PCR primer or probe comprises the sequence of SEQ ID NO:12.

32. (Currently amended) The kit of claim [[29]] 30, wherein said first ~~at least one~~ PCR primer or probe comprises the sequence of SEQ ID NO:11.

33. (Cancelled)

34. (Currently amended) A method for screening the genomic DNA of seeds for the presence of MS-B2, which method comprises detecting, in the genomic DNA of seeds, an MS-B2 specific region comprising the insertion site of MS-B2, using a polymerase chain reaction with a first specific primer or probe which comprises at least 16 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in ~~hybridizes to~~ bases 1-234 of SEQ ID NO:8, or the complement thereof, or from the 3' flanking region of MS-B2, comprised in ~~to~~ bases 194-416 of SEQ ID NO:10, or the complement thereof, ~~of MS-B2~~, and a second specific primer or probe which comprises at least 16 consecutive nucleotides from the foreign DNA in MS-B2, or the complement thereof, said foreign DNA corresponding to a sequence within SEQ ID NO:1; and thus confirming the presence of MS-B2 if the MS-B2 specific DNA sequence is so detected in said seeds ~~samples of seed lots~~.

35. (Currently amended) A method for screening the genomic DNA of seeds for the absence of MS-B2, which method comprises carrying out, in the genomic DNA of seeds, a polymerase chain reaction ~~Polymerase Chain Reaction or Southern Blot~~ using a first specific primer or probe which comprises at least 16 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in ~~hybridizes to~~ bases 1-234 of SEQ ID NO:8, or the complement thereof, or from the 3' flanking region of MS-B2, comprised in ~~to~~ bases 194-416 of SEQ ID NO:10, or the complement thereof; ~~of MS-B2~~, and a second specific primer or probe which comprises at least 16 consecutive nucleotides from the foreign DNA in MS-B2, or the complement thereof, said foreign DNA corresponding to a sequence within SEQ ID NO:1; and not detecting the

presence of MS-B2 specific DNA on an agarose gel ~~or Southern Blot membrane~~, thus confirming the absence of MS-B2 in said seeds.

36. (Currently amended) A method for identifying a *Brassica* plant, or cell or tissue thereof, or *Brassica* plant material not comprising elite event MS-B2, which method comprises establishing whether the genomic DNA of the plant, or cell, or tissue thereof, or transgenic plant material cannot amplify a DNA fragment of between 100 and 300 nucleotides using ~~performing~~ a polymerase chain reaction (PCR) with a first primer or probe ~~at least two primers, one of~~ which comprises at least 16 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in ~~recognizes~~ bases 1-234 of SEQ ID NO:8, or the complement thereof, or from the 3' flanking region of MS-B2, comprised in bases 194-416 of SEQ ID NO:10, or the complement thereof; ~~of MS-B2~~, and a second specific primer or probe which comprises at least 16 consecutive nucleotides from the foreign DNA in MS-B2, or the complement thereof, said foreign DNA corresponding to ~~another of which recognizes~~ a sequence within SEQ ID NO:1; and thus identifying a Brassica plant, or cell or tissue thereof, or transgenic plant material not comprising elite event MS-B2, if said genomic DNA cannot amplify the DNA fragment using PCR with the primers~~, and detecting the absence of a DNA fragment of between 160 and 200 base pairs on an agarose gel~~.

37. (New) The method of claim 24, wherein said first specific primer or probe comprises 20 to 24 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in bases 1-234 of SEQ ID NO:8, or the complement thereof, or from the 3' flanking region of MS-B2, comprised in bases 194-416 of SEQ ID NO:10, or the complement thereof, and said second specific primer or probe comprises 20-24 consecutive nucleotides from the foreign DNA in MS-B2, or the complement thereof, said foreign DNA corresponding to a sequence within SEQ ID NO:1.

38. (New) The method of claim 24, wherein said first specific primer or probe comprises the sequence of SEQ ID NO:11.

39. (New) The method of claim 24, wherein said first specific primer or probe comprises at least 16 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in bases 1-234 of SEQ ID NO:8, or the complement thereof.

40. (New) The kit of claim 30, wherein said first PCR primer or probe comprises 20-24 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in bases 1-234 of

SEQ ID NO:8, or the complement thereof, or from the 3' flanking region of MS-B2, comprised in bases 194-416 of SEQ ID NO:10, or the complement thereof, and wherein said second specific primer or probe comprises 20-24 consecutive nucleotides from foreign DNA in MS-B2, or the complement thereof, said foreign DNA corresponding to a sequence within SEQ ID NO:1.

41, (New) The kit of claim 30, wherein said first PCR primer or probe comprises at least 16 consecutive nucleotides from the 5' flanking region of MS-B2, comprised in bases 1-234 of SEQ ID NO:8, or the complement thereof.

42. (New) The kit of claim 30, wherein said first PCR primer or probe comprises at least 16 consecutive nucleotides from the 3' flanking region of MS-B2, comprised in bases 194-416 of SEQ ID NO:10, or the complement thereof.